



IFW16

RAW SEQUENCE LISTING

DATE: 08/24/2004

PATENT APPLICATION: US/08/958,570A

TIME: 10:11:59

Input Set : N:\Crf3\RULE60\08958570A.raw

Output Set: N:\CRF4\08242004\H958570A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Gregory, Richard J.

3 Wills, Ken N.

4 Maneval, Daniel C.

5 (ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and

6 Methods of Use

7 (iii) NUMBER OF SEQUENCES: 9

8 (iv) CORRESPONDENCE ADDRESS:

9 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

10 (B) STREET: Two Embarcadero Center, Eighth Floor

11 (C) CITY: San Francisco

12 (D) STATE: California

13 (E) COUNTRY: USA

14 (F) ZIP: 94111-3834

15 (v) COMPUTER READABLE FORM:

16 (A) MEDIUM TYPE: Floppy disk

17 (B) COMPUTER: IBM PC compatible

18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

19 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:

C--> 21 (A) APPLICATION NUMBER: US/08/958,570A

C--> 22 (B) FILING DATE: 28-Oct-1997

23 (C) CLASSIFICATION:

24 (vii) PRIOR APPLICATION DATA:

W--> 25 (A) APPLICATION NUMBER: US/08/328,673

26 (B) FILING DATE: 25-Oct-1994

W--> 27 (A) APPLICATION NUMBER: US 08/142,669

28 (B) FILING DATE: 25-OCT-1993

W--> 29 (A) APPLICATION NUMBER: US 08/233,669

30 (B) FILING DATE: 26-APR-1994

31 (viii) ATTORNEY/AGENT INFORMATION:

32 (A) NAME: Smith, Timothy S.

33 (B) REGISTRATION NUMBER: 35,367

34 (C) REFERENCE/DOCKET NUMBER: 016930-000920US

35 (ix) TELECOMMUNICATION INFORMATION:

36 (A) TELEPHONE: (415) 576-0200

37 (B) TELEFAX: (415) 576-0300

38 (2) INFORMATION FOR SEQ ID NO: 1:

39 (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 25 base pairs

41 (B) TYPE: nucleic acid

42 (C) STRANDEDNESS: single

ENTERED

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43          (D) TOPOLOGY: linear
W--> 44      (ii) MOLECULE TYPE: DNA
45          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
46          CGCCACCGAG GGACCTGAGC GAGTC
48 (2) INFORMATION FOR SEQ ID NO: 2:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 20 base pairs
51          (B) TYPE: nucleic acid
52          (C) STRANDEDNESS: single
53          (D) TOPOLOGY: linear
W--> 54      (ii) MOLECULE TYPE: DNA
55          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
56          TTCTGGGAAG GGACAGAAGA
58 (2) INFORMATION FOR SEQ ID NO: 3:
59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 25 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: single
63          (D) TOPOLOGY: linear
W--> 64      (ii) MOLECULE TYPE: DNA
65          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
66          CGCGCTAGCT CTGCCCAAA GAGCT
68 (2) INFORMATION FOR SEQ ID NO: 4:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 39 base pairs
71          (B) TYPE: nucleic acid
72          (C) STRANDEDNESS: single
73          (D) TOPOLOGY: linear
W--> 74      (ii) MOLECULE TYPE: DNA
75          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
76          CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGAAG
78 (2) INFORMATION FOR SEQ ID NO: 5:
79      (i) SEQUENCE CHARACTERISTICS:
80          (A) LENGTH: 35 base pairs
81          (B) TYPE: nucleic acid
82          (C) STRANDEDNESS: single
83          (D) TOPOLOGY: linear
W--> 84      (ii) MOLECULE TYPE: DNA
85          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
86          CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC
88 (2) INFORMATION FOR SEQ ID NO: 6:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 33 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: linear
W--> 94      (ii) MOLECULE TYPE: DNA
95          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
96          CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA

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98 (2) INFORMATION FOR SEQ ID NO: 7:

99 (i) SEQUENCE CHARACTERISTICS:

100 (A) LENGTH: 2995 base pairs

101 (B) TYPE: nucleic acid

102 (C) STRANDEDNESS: single

103 (D) TOPOLOGY: linear

104 (ii) MOLECULE TYPE: cDNA

105 (ix) FEATURE:

106 (A) NAME/KEY: CDS

107 (B) LOCATION: 139..2925

108 (D) OTHER INFORMATION: /product= "RB"

109 /note= "retinoblastoma tumor suppressor"

110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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111 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CCGGAGTCGG GAGAGGACGG      60
112 GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCGCGCGCT CCTCCACAGC TCGCTGGCTC      120
113 CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC      171
114                               Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
115                               1           5           10
116 ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC      219
117 Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
118           15           20           25
119 CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT      267
120 Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
121           30           35           40
122 CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA      315
123 Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
124           45           50           55
125 TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG      363
126 Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
127           60           65           70           75
128 TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT      411
129 Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
130           80           85           90
131 ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA      459
132 Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
133           95           100           105
134 GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC      507
135 Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
136           110           115           120
137 ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT      555
138 Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
139           125           130           135
140 ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT      603
141 Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
142           140           145           150           155
143 GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT      651
144 Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
145           160           165           170
146 ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT      699

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147	Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
148	175 180 185	
149	GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	747
150	Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
151	190 195 200	
152	GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	795
153	Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
154	205 210 215	
155	CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	843
156	Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
157	220 225 230 235	
158	AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	891
159	Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160	240 245 250	
161	ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	939
162	Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
163	255 260 265	
164	GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	987
165	Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
166	270 275 280	
167	AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035
168	Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
169	285 290 295	
170	ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	1083
171	Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
172	300 305 310 315	
173	AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	1131
174	Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
175	320 325 330	
176	GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
177	Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
178	335 340 345	
179	ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
180	Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
181	350 355 360	
182	GAA GAG GTG AAT GTA ATT CTT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
183	Glu Glu Val Asn Val Ile Leu Pro His Thr Pro Val Arg Thr Val Met	
184	365 370 375	
185	AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
186	Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
187	380 385 390 395	
188	CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
189	Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
190	400 405 410	
191	AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
192	Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
193	415 420 425	
194	GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
195	Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	

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196	430	435	440	
197	CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC			1515
198	Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser			
199	445	450	455	
200	ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA			1563
201	Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys			
202	460	465	470	475
203	CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT			1611
204	Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu			
205	480	485	490	
206	GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT			1659
207	Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp			
208	495	500	505	
209	TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA			1707
210	Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu			
211	510	515	520	
212	AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA			1755
213	Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu			
214	525	530	535	
215	GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT			1803
216	Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His			
217	540	545	550	555
218	CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT			1851
219	Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp			
220	560	565	570	
221	CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA			1899
222	Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu			
223	575	580	585	
224	TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA			1947
225	Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala			
226	590	595	600	
227	GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT			1995
228	Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr			
229	605	610	615	
230	ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC			2043
231	Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala			
232	620	625	630	635
233	TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT			2091
234	Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr			
235	640	645	650	
236	AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA			2139
237	Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu			
238	655	660	665	
239	CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT			2187
240	Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu			
241	670	675	680	
242	TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT			2235
243	Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His			
244	685	690	695	

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/958,570A

DATE: 08/24/2004

TIME: 10:12:00

Input Set : N:\Crf3\RULE60\08958570A.raw

Output Set: N:\CRF4\08242004\H958570A.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:44 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:54 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:64 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:84 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:94 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6